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## RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/897,898

TIME: 17:40:08

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3 <110> APPLICANT: DECKERS, HARM M.  
4 VAN ROOIJEN, GIJS  
5 BOOTHE, JOSEPH  
6 GOLL, JANIS  
7 MOLONEY, MAURICE M.  
8 DALMIA, BIPIN K.  
10 <120> TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL  
11 BODY BASED PRODUCTS  
13 <130> FILE REFERENCE: 034547/0104  
15 <140> CURRENT APPLICATION NUMBER: 09/897,898  
C--> 16 <141> CURRENT FILING DATE: 2001-09-21  
18 <150> PRIOR APPLICATION NUMBER: 09/577,147  
19 <151> PRIOR FILING DATE: 2000-05-24  
21 <150> PRIOR APPLICATION NUMBER: 09/448,600  
22 <151> PRIOR FILING DATE: 1999-11-24  
24 <150> PRIOR APPLICATION NUMBER: 09/084,777  
25 <151> PRIOR FILING DATE: 1998-05-27  
27 <150> PRIOR APPLICATION NUMBER: 60/047,753  
28 <151> PRIOR FILING DATE: 1997-05-27  
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31 <151> PRIOR FILING DATE: 1997-05-28  
33 <150> PRIOR APPLICATION NUMBER: 60/075,863  
34 <151> PRIOR FILING DATE: 1998-02-25  
36 <150> PRIOR APPLICATION NUMBER: 60/075,864  
37 <151> PRIOR FILING DATE: 1998-02-25  
39 <160> NUMBER OF SEQ ID NOS: 24  
41 <170> SOFTWARE: PatentIn Ver. 2.1  
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44 <211> LENGTH: 1002  
45 <212> TYPE: DNA  
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48 <220> FEATURE:  
49 <221> NAME/KEY: CDS  
50 <222> LOCATION: (1)..(999)  
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53 <223> OTHER INFORMATION: Description of Unknown Organism: Published NADPH *OK*  
54 thioredoxin reductase  
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59 1 5 10 15  
61 ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt 96  
62 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu  
63 20 25 30  
65 aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 144  
66 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly  
67 35 40 45

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73 gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg 240
74 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
75 65                      70                      75                      80
77 gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat 288
78 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
79                      85                      90                      95
81 ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc 336
82 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
83      100                      105                      110
85 gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc 384
86 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
87      115                      120                      125
89 ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc 432
90 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
91      130                      135                      140
93 tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa 480
94 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
95 145                      150                      155                      160
97 cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac 528
98 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
99      165                      170                      175
101 ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat 576
102 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
103      180                      185                      190
105 gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct 624
106 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
107      195                      200                      205
109 aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat 672
110 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
111      210                      215                      220
113 gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc 720
114 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
115 225                      230                      235                      240
117 gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt 768
118 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
119      245                      250                      255
121 cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg 816
122 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
123      260                      265                      270
125 gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc 864
126 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
127      275                      280                      285
129 gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc 912
130 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
131      290                      295                      300
133 atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat 960

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134 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
135 305                      310                      315                      320
137 tac tta caa gag att gga tct cag caa ggt aag agt gat tga          1002
138 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
139                      325                      330
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144 <212> TYPE: DNA
145 <213> ORGANISM: Arabidopsis sp.
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (1)..(999)
151 <400> SEQUENCE: 2
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154 1                      5                      10                      15
156 ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt      96
157 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
158                      20                      25                      30
160 aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt      144
161 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
162                      35                      40                      45
164 ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca      192
165 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
166 50                      55                      60
168 gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg      240
169 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
170 65                      70                      75                      80
172 gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat      288
173 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
174                      85                      90                      95
176 ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc      336
177 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
178                      100                      105                      110
180 gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc      384
181 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
182                      115                      120                      125
184 ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc      432
185 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
186                      130                      135                      140
188 tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa      480
189 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
190 145                      150                      155                      160
192 cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac      528
193 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
194                      165                      170                      175
196 ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat      576
197 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
198                      180                      185                      190

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200 gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct 624
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202      195      200      205
204 aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat 672
205 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
206      210      215      220
208 gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc 720
209 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
210 225      230      235      240
212 gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt 768
213 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
214      245      250      255
216 cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg 816
217 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
218      260      265      270
220 gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc 864
221 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
222      275      280      285
224 gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc 912
225 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
226      290      295      300
228 atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat 960
229 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
230 305      310      315      320
232 tac tta caa gag att gga tct cag caa ggt aag agt gat tga 1002
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234      325      330
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238 <211> LENGTH: 333
239 <212> TYPE: PRT
240 <213> ORGANISM: Arabidopsis sp.
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249 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
250      35      40      45
252 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
253      50      55      60
255 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
256 65      70      75      80
258 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
259      85      90      95
261 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
262      100      105      110
264 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
265      115      120      125
267 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile

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268      130      135      140
270 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
271 145      150      155      160
273 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
274      165      170      175
276 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
277      180      185      190
279 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
280      195      200      205
282 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
283 210      215      220
285 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
286 225      230      235      240
288 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
289      245      250      255
291 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
292      260      265      270
294 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
295      275      280      285
297 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
298 290      295      300
300 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
301 305      310      315      320
303 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
304      325      330
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308 <211> LENGTH: 333
309 <212> TYPE: PRT
310 <213> ORGANISM: Unknown Organism
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Description of Unknown Organism: Published NADPH
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316 <400> SEQUENCE: 4
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323 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
324      35      40      45
326 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
327 50      55      60
329 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
330 65      70      75      80
332 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
333      85      90      95
335 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
336      100      105      110
338 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
339      115      120      125

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VERIFICATION SUMMARY

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